

Partners launch DREAM Toxicogenetics Challenge

An innovative crowdsourced computational [challenge](https://www.synapse.org/#!/Synapse:syn1761567),
(<https://www.synapse.org/#!/Synapse:syn1761567>)
the DREAM Toxicogenetics Challenge, launched June 11 with an announcement by
[Sage Bionetworks](http://sagebase.org/2013/06/04/may-the-best-model-win-2/).

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The goal of the three-month challenge is to find better ways to predict the toxicity of chemicals, to increase understanding of how a person's individual genetics can influence cytotoxic response of exposure to widely used chemicals.

The challenge is being led and organized by scientists from Sage Bionetworks,
[DREAM](http://www.the-dream-project.org/)

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(Dialogue for Reverse Engineering Assessments and Methods), the University of North Carolina at Chapel Hill (UNC), NIEHS, and the NIH National Center for Advancing Translational Sciences (NCATS). These groups have generated population-scale toxicity data in a human *in vitro* model system.

The partners utilized human cell lines from the 1000 Genomes Project, which consists of correlated genomic data and cell lines collected from individuals representing nine distinct populations with defined genetic heterogeneity. The NIEHS-NCATS-UNC team has conducted the largest ever population-based *in vitro* cytotoxicity study, by evaluating the extent of cytotoxicity induced by 179 common pharmaceutical or important environmental chemicals in 1086 human lymphoblastoid cell lines. The challenge is asking a wide range of researchers to use the genomic and cytotoxicity data to build models that can predict variation in individual response to a chemical, based on genomic data.

Challenges such as this engage diverse communities of scientists to competitively solve a specific problem in a given time period, by placing scientific data, tools, and the resulting predictive models into an open commons or workspace — in effect, crowdsourcing data analysis.

Those interested in participating in this challenge, and two others, can sign up at a dedicated [Web page](https://www.synapse.org/#!/Challenges:DREAM8).

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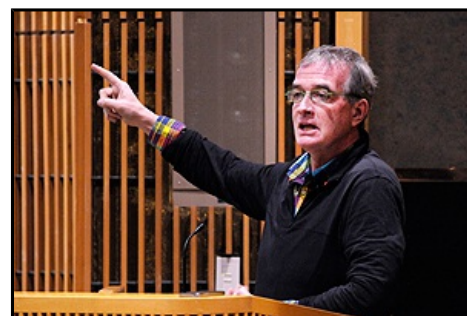
The challenge will close on Sept. 15 and the top-scoring team(s) will be announced at the [sixth annual RECOMB/ISCB conference on Regulatory and Systems Genomics, with DREAM Challenges](http://www.iscb.org/recomb-regsysgen2013),

(<http://www.iscb.org/recomb-regsysgen2013>)

Nov. 8-12 in Toronto.

A big data approach to understanding chemical toxicity

"Predicting how different people or groups of people will respond to certain chemicals is difficult to determine, but important for protecting the public's health," said [Raymond Tice, Ph.D.](#), who heads the NTP Biomolecular Screening Branch at NIEHS and is leading an NTP initiative to



Co-founder, president, and director of Sage Bionetworks [Stephen Friend, M.D., Ph.D.](http://sagebase.org/our-leadership/), (<http://sagebase.org/our-leadership/>) explored the challenge concept during a talk at NIEHS (see [story](#)) earlier this year. (Photo courtesy of Steve McCaw)



Deary provides leadership in the effort to define, plan, and evaluate scientific data and knowledge management approaches in environmental health. (Photo courtesy of Steve McCaw)

develop a paradigm of predictive toxicology using high-throughput screening. “This challenge represents a novel partnership and a novel approach to addressing, more effectively and efficiently, big data problems in environmental health science,” added [Allen Dearry, Ph.D.](#), director of the NIEHS Office of Scientific Information Management, which coordinated interaction with Sage/DREAM.

“We are delighted to partner with Sage/DREAM, to release this unique dataset obtained through a broad partnership with NIEHS and NCATS,” said [Ivan Rusyn, M.D., Ph.D.](#), (http://www2.sph.unc.edu/index.php?option=com_profiles&profileAction=ProfDetail&pid=702665970)

professor of environmental sciences and engineering at the UNC Gillings School of Global Public Health. “The collaboration with Sage/DREAM is an important extension of our ongoing partnership with NIEHS and UNC,” added [Anton Simeonov, Ph.D.](#), (http://www.aaps.org/Meetings_and_Professional_Development/Conference_Mini_Sites/2013_AAPS_National_Biotechnology_Conference/content/Anton_Simeonov,_Ph_D_/) NCATS acting scientific director of discovery innovation.

This is the type of challenge that all of the partners are most interested in running — those with the potential to provide powerful scientific insights and meaningful public impact. Toxicity testing that monitors health risks posed to humans through chemical exposure is a crucial component of public health. Yet, for every chemical that has been tested for toxicity, there are thousands that remain untested.

To address this backlog, toxicologists are interested in leveraging the dramatic technological advances in molecular biology and computer science that now make it possible to use high throughput *in vitro* biochemical and cell-based assays with banks of genomic data for toxicological testing. The challenge aims to advance the pace of using and analyzing such complex data, in order to accelerate the generation of useful information for the scientific and public health communities.



Tice is the NTP lead on the Tox21 consortium, a partnership of NIEHS, the U.S. Environmental Protection Agency, U.S. Food and Drug Administration, and NIH Chemical Genomics Center. (Photo courtesy of Steve McCaw)



Rusyn is a long-term NIEHS grantee and a leader in the field of toxicogenomics. (Photo courtesy of UNC)



Simeonov is a key member of the NCATS team of scientists conducting clinical and translational research to transform laboratory discoveries into new therapies for patients. (Photo courtesy of NIH)

Challenges open June 11 to Sept. 15

The NIEHS-NCATS-UNC DREAM Toxicogenetics Challenge is one of [three challenges](https://www.synapse.org/#!/Challenges:DREAM8) (<https://www.synapse.org/#!/Challenges:DREAM8>)

that Sage Bionetworks and DREAM opened to the public. The two other challenges involve breast cancer networks and whole cell model parameters.

- **The Heritage Provider Network-DREAM Breast Cancer Network Inference Challenge** —Participants in this challenge will be provided with an extensive proteomics time-course dataset on four breast cancer cell lines and tasked with analyzing these data to solve three sub-challenges — building network models that represent the active cell signaling pathways in breast cancer; predicting the dynamic response of various phospho-proteins to drug perturbations; and proposing novel strategies to visualize these high dimensional data.
- **The Whole-Cell Parameter Estimation DREAM Challenge** — Participants will be provided with a whole cell model of the sexually transmitted pathogen *Mycoplasma genitalium* and tasked with estimating the model parameters, from simulated data, for specific biological processes. The simulated data to be provided represents possible measurements in actual experiments, as participants interact with a credit system to purchase this data on demand, with the aim to refine the parameters under estimation.

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